```
                              GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:          July 28, 2004, 11:35:32 ; Search time 9.10345 Seconds
                                            (without alignments)
                                            84.532 Million cell updates/sec


Title:
Perfect score:   SEQ3
Sequence:        43
                 1 qppraaiy 8

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:        0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 75 summaries

Database  :      PIR_78:*
                 1:  pir1:*
                 2:  pir2:*
                 3:  pir3:*
                 4:  pir4:*


         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.


                                   SUMMARIES

Result           %        Query
No.     Score    Match    Length  DB    ID             Description
------  -----    -----    ------  --    --             -----------


No matches found


Search completed: July 28, 2004, 11:59:05
Job time : 9.10345 secs
```

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on:          July 28, 2004, 11:34:37 ; Search time 5.10345 Seconds
                                           (without alignments)
                                           81.623 Million cell updates/sec

Title:
Perfect score:   43
Sequence:        SEQ3
                 1 qppraaiy 8

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:      0

Database :       SwissProt_42.*

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 75 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

Result           Query
No.     Score   Match Length DB  ID                    Description
------  -----   ------------ --- --                    -----------

No matches found

Search completed: July 28, 2004, 11:49:10
Job time : 5.10345 secs

```
                    GenCore version 5.1.6
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OM protein - protein search, using sw model


Run on:          July 28, 2004, 11:35:02 ; Search time 30.4828 Seconds
                                            (without alignments)
                                            82.806 Million cell updates/sec


Title:
Perfect score:   SEQ3
Sequence:        43
                 1 qppraaiy 8


Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5


Searched:        1017041 seqs, 315518202 residues


Total number of hits satisfying chosen parameters:     0


Post-processing: Minimum Match 100%
Minimum DB seq length: 0                     Maximum Match 100%
Maximum DB seq length: 2000000000            Listing first 75 summaries


Database :       SPTREMBL_25:*
                 1:  sp_archea:*
                 2:  sp_bacteria:*
                 3:  sp_fungi:*
                 4:  sp_human:*
                 5:  sp_invertebrate:*
                 6:  sp_mammal:*
                 7:  sp_mhc:*
                 8:  sp_organelle:*
                 9:  sp_phage:*
                 10: sp_plant:*
                 11: sp_rodent:*
                 12: sp_virus:*
                 13: sp_vertebrate:*
                 14: sp_unclassified:*
                 15: sp_rvirus:*
                 16: sp_bacteriap:*
                 17: sp_archeap:*


Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.


                                 SUMMARIES

Result                 %    Query
   No.   Score   Match Length DB   ID              Description
-------  -----   ----- ------ --   --              -----------


No matches found


Search completed: July 28, 2004, 11:56:43
Job time : 30.4828 secs
```

```
OM protein - protein search, using sw model

                              GenCore version 5.1.6
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Run on:            July 28, 2004, 11:33:47 ; Search time 46.1379 Seconds
                              (without alignments)
                              48.992 Million cell updates/sec

Title:             SEQ3
Perfect score:     43
Sequence:          1 qppraaiy 8

Scoring table:
                   BLOSUM62
                   Gapop 10.0 , Gapext 0.5
Searched:          1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters:      2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:   Minimum Match 100%
                   Maximum Match 100%
                   Listing first 75 summaries

Database :         A_Geneseq_29Jan04:*
                   1: geneseqp1980s:*
                   2: geneseqp1990s:*
                   3: geneseqp2000s:*
                   4: geneseqp2001s:*
                   5: geneseqp2002s:*
                   6: geneseqp2003as:*
                   7: geneseqp2003bs:*
                   8: geneseqp2004s:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                                           SUMMARIES

Result               %     Query
  No.    Score   Match   Length   DB   ID              Description
------   -----   -----   ------   --   ---------       ---------------
  1       43    100.0      8       3   AAB19055        Aab19055 Amino aci
  2       43    100.0      9       2   AAY28517        Aay28517 Beta-1 in

                                          ALIGNMENTS

RESULT 1
AAB19055
ID   AAB19055 standard; peptide; 8 AA.
XX
AC   AAB19055;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Amino acid sequence of a beta1-integrin inhibitor.
XX
KW   Beta1-integrin inhibitor; leukocyte mediated tissue destruction;
KW   central nervous system ischemic injury; myocardial infarction;
KW   beta1-integrin; angioplasty; surgical incision; injury-related trauma;
KW   transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.
XX
OS   Synthetic.
XX
PN   WO200056350-A2.
XX
```

```
XX
PD   28-SEP-2000.
XX
PF   22-MAR-2000;  2000WO-US007680.
XX
PR   22-MAR-1999;  99US-0125634P.
PR   24-NOV-1999;  99US-0167538P.
XX
PA   (MINU )  UNIV MINNESOTA.
PA   (TEXA )  UNIV TEXAS SYSTEM.
PA   (SENT-)  SENTRON MEDICAL INC.
XX
PI   Mccarthy JB, Mileski WJ, Jamieson GA, Low WC, Sawchuk RJ;
PI   Furcht LT;
XX
DR   WPI; 2000-656062/63.
XX
PT   Inhibition of inflammatory leukocyte mediated destruction of tissue in a
PT   patient, comprises administering a peptide inhibitor of beta1-integrin,
PT   useful for treatment of e.g. cancer and osteoporosis.
XX
PS   Claim 3; Page 38; 61pp; English.
XX
CC   AAB19054-67 represent beta1-integrin inhibitors. The peptides inhibit
CC   beta1-integrin which is responsible for leukocyte mediated tissue
CC   destruction. The peptides are useful for inhibiting inflammatory
CC   leukocyte mediated destruction of tissue which occurs as a result of
CC   central nervous system (CNS) ischemic injury, myocardial infarction,
CC   angioplasty, surgical incision, injury-related trauma, and/or transplant
CC   reperfusion, exposure to heat, cold, light, electricity and/or chemicals.
CC   They are also useful for the treatment of stroke, a burn type injury,
CC   cancer, and osteoporosis
XX
SQ   Sequence 8 AA;

Qy           1 QPPRAAIY 8
               ||||||||
Db           1 QPPRAAIY 8

Query Match             100.0%;  Score 43;  DB 3;  Length 8;
Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


RESULT 2
AAY28517
ID   AAY28517 standard; peptide; 9 AA.
XX
AC   AAY28517;
XX
DT   19-OCT-1999  (first entry)
XX
DE   Beta-1 integrin cell adhesion modulator analogue #8.
XX
KW   Beta 1 integrin dependent cell adhesion; LipAr motif; tumour;
KW   C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
XX
OS   Synthetic.
XX
PN   WO9937669-A1.
XX
PD   29-JUL-1999.
XX
PF   21-JAN-1999;  99WO-US001236.
XX
PR   22-JAN-1998;  98US-0072119P.
PR   12-AUG-1998;  98US-0096210P.
PR   12-AUG-1998;  98US-0096212P.
XX
PA   (MINU )  UNIV MINNESOTA.
XX
PI   Mccarthy JB, Furcht LT, Brienzo A;
XX
```

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OM protein - protein search, using sw model

Run on:            July 28, 2004, 11:56:53 ; Search time 38.8966 Seconds
                                             (without alignments)
                                             64.516 Million cell updates/sec

Title:             SEQ3
Perfect score:     43
Sequence:          1 qppraaiy 8

Scoring table:     BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched:          1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters:     0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 75 summaries

Database :       Published_Applications_AA:*
       1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
       2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
       3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
       4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
       5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
       6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
       7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
       8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
       9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
      10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
      11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
      12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
      13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
      14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
      15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
      16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
      17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
      18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

Result                %        Query
No.     Score    Match Length  DB   ID                     Description
------  -----    ------------  --   --                     -----------

No matches found

Search completed: July 28, 2004, 12:58:37
Job time : 38.8966 secs

OM protein - protein search, using sw model

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Run on:          July 28, 2004, 11:36:28 ; Search time 12.4138 Seconds
                                            (without alignments)
                                            33.270 Million cell updates/sec

Title:
Perfect score:   43
Sequence:        1 qppraaiy 8

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:     0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
                 Maximum Match 100%
                 Listing first 75 summaries

Database :       Issued_Patents_AA:*
                 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
                 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
                 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
                 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
                 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

                 Pred. No. is the number of results predicted by chance to have a
                 score greater than or equal to the score of the result being printed,
                 and is derived by analysis of the total score distribution.

                                    SUMMARIES

Result           %       Query
No.     Score   Match   Length  DB    ID              Description
------  -----   -----   ------  --    --              -----------

No matches found

Search completed: July 28, 2004, 12:02:17
Job time : 12.4805 secs